

SEQUENCE LISTING

<110> The Walter and Eliza Hall Institute of Medical Research

<120> A novel phosphoprotein

<130> 2589867/EJH

<150> AU 2002953341

<151> 2002-12-13

<140> Not yet available

<141> 2002-12-12

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 13

<212> PRT

<213> peptide

<400> 1

Glu Ser Ala Val Ala Glu Ser Arg Glu Glu Arg Met Gly
1 5 10

<210> 2

<211> 18

<212> PRT

<213> peptide

<400> 2

Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu
1 5 10 15

Ser Arg

<210> 3

<211> 18

<212> PRT

<213> peptide

<400> 3

Arg Arg Ala Ala Ser Met Asp Asn Asn Ser Lys Phe Ala Lys Ser Arg
1 5 10 15

Ser Arg

<210> 4
 <211> 876
 <212> DNA
 <213> phosphoprotein

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 gtgggctgga acctgacctc tagcagggct ggggtgtctg tctgggtgca ggctgtggag 180
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 aactctacg acgtcctaca cgacattgag taccgcaaga aatgggacag caacgtcatt 300
 gagacttttg acatcgcccg cttgacagtc aacgctgacg tgggctatta ctccctggagg 360
 tgtccaagc ccctgaagaa ccgtgatgtc atcacccctcc gctcctggct ccccatgggc 420
 gctgattaca tcattatgaa ctactcagtc aaacatccca aatacccacc tcggaaagac 480
 ttgggtccgag ctgtgtccat ccagacgggc tacctcatcc agagcacagg gccaagagc 540
 tgcgtcatca cctacctggc ccaggtggac cccaaaggct ccttaccxaa gtgggtggtg 600
 aataaatctt ctcaattcct ggctcccaag gccatgaaga agatgtacaa ggcgtgcctc 660
 aagtaccccg agtggaacaa gaagcacctg cctcacttca agccgtggct gcacccggag 720
 cagagcccggt tgccgagcct ggcgctgtcg gagctgtcgg tgcagcatgc ggactcactg 780
 gagaacatcg acgagagcgc ggtggccgag agcagagagg agcggatggg cggcgcgggc 840
 ggcgagggca gcgacgacga cacctcgctc acctga 876

<210> 5
 <211> 291
 <212> PRT
 <213> phosphoprotein

<400> 5

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			20					25					30		
Phe	Arg	Ser	Glu	Cys	Glu	Ala	Glu	Val	Gly	Trp	Asn	Leu	Thr	Tyr	Ser
		35					40					45			
Arg	Ala	Gly	Val	Ser	Val	Trp	Val	Gln	Ala	Val	Glu	Met	Asp	Arg	Thr
		50				55					60				
Leu	His	Lys	Ile	Lys	Cys	Arg	Met	Glu	Cys	Cys	Asp	Val	Pro	Ala	Glu
65					70					75					80
Thr	Leu	Tyr	Asp	Val	Leu	His	Asp	Ile	Glu	Tyr	Arg	Lys	Lys	Trp	Asp
				85					90					95	

Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu Thr Val Asn Ala
100 105 110

Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro Leu Lys Asn Arg
115 120 125

Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly Ala Asp Tyr Ile
130 135 140

Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro Pro Arg Lys Asp
145 150 155 160

Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu Ile Gln Ser Thr
165 170 175

Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln Val Asp Pro Lys
180 185 190

Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser Gln Phe Leu Ala
195 200 205

Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu Lys Tyr Pro Glu
210 215 220

Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp Leu His Pro Glu
225 230 235 240

Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu Ser Val Gln His
245 250 255

Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu Ser Arg
260 265 270

Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser Asp Asp Asp Thr
275 280 285

Ser Leu Thr
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<210> 6
<211> 359
<212> PRT
<213> human

<400> 6

Met Ser Thr Arg Ala Lys Lys Leu Arg Arg Ile Trp Arg Ile Leu Glu
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Glu Glu Glu Ser Val Ala Gly Ala Val Gln Thr Leu Leu Leu Arg Ser
20 25 30

Gln Glu Gly Gly Val Thr Ser Ala Ala Ala Ser Thr Leu Ser Glu Pro
35 40 45

Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg Ala Leu Gly Leu
50 55 60

Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly
65 70 75 80

Pro	Arg	Pro	Val	Leu	Gly	Arg	Glu	Ser	Val	Gln	Val	Pro	Asp	Asp	Gln
				85					90					95	
Asp	Phe	Arg	Ser	Phe	Arg	Ser	Glu	Cys	Glu	Ala	Glu	Val	Gly	Trp	Asn
			100					105					110		
Leu	Thr	Tyr	Ser	Arg	Ala	Gly	Val	Ser	Val	Trp	Val	Gln	Ala	Val	Glu
		115					120					125			
Met	Asp	Arg	Thr	Leu	His	Lys	Ile	Lys	Cys	Arg	Met	Glu	Cys	Cys	Asp
	130					135					140				
Val	Pro	Ala	Glu	Thr	Leu	Tyr	Asp	Val	Leu	His	Asp	Ile	Glu	Tyr	Arg
145					150					155					160
Lys	Lys	Trp	Asp	Ser	Asn	Val	Ile	Glu	Thr	Phe	Asp	Ile	Ala	Arg	Leu
				165					170					175	
Thr	Val	Asn	Ala	Asp	Val	Gly	Tyr	Tyr	Ser	Trp	Arg	Cys	Pro	Lys	Pro
			180					185					190		
Leu	Lys	Asn	Arg	Asp	Val	Ile	Thr	Leu	Arg	Ser	Trp	Leu	Pro	Met	Gly
		195					200					205			
Ala	Asp	Tyr	Ile	Ile	Met	Asn	Tyr	Ser	Val	Lys	His	Pro	Lys	Tyr	Pro
	210					215					220				
Pro	Arg	Lys	Asp	Leu	Val	Arg	Ala	Val	Ser	Ile	Gln	Thr	Gly	Tyr	Leu
225					230					235					240
Ile	Gln	Ser	Thr	Gly	Pro	Lys	Ser	Cys	Val	Ile	Thr	Tyr	Leu	Ala	Gln
				245					250					255	
Val	Asp	Pro	Lys	Gly	Ser	Leu	Pro	Lys	Trp	Val	Val	Asn	Lys	Ser	Ser
			260					265					270		
Gln	Phe	Leu	Ala	Pro	Lys	Ala	Met	Lys	Lys	Met	Tyr	Lys	Ala	Cys	Leu
		275					280					285			
Lys	Tyr	Pro	Glu	Trp	Lys	Gln	Lys	His	Leu	Pro	His	Phe	Lys	Pro	Trp
	290					295					300				
Leu	His	Pro	Glu	Gln	Ser	Pro	Leu	Pro	Ser	Leu	Ala	Leu	Ser	Glu	Leu
305					310					315					320
Ser	Val	Gln	His	Ala	Asp	Ser	Leu	Glu	Asn	Ile	Asp	Glu	Ser	Ala	Val
				325					330					335	

Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser
340 345 350

Asp Asp Asp Thr Ser Leu Thr
355

<210> 7
<211> 214
<212> PRT
<213> human

<400> 7

Met Glu Leu Ala Ala Gly Ser Phe Ser Glu Glu Gln Phe Trp Glu Ala
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Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu
20 25 30

Leu Val Glu Thr Ser Gly Ile Ser Ile Tyr Arg Leu Leu Asp Lys Lys
35 40 45

Thr Gly Leu His Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
50 55 60

Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
65 70 75 80

Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
85 90 95

Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
100 105 110

Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg
115 120 125

Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
130 135 140

Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
145 150 155 160

Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
165 170 175

Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
180 185 190

Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln
195 200 205

Asn Tyr Leu Lys Lys Thr
210